

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:26:04 ; Search time 29.37 Seconds
(without alignments)
24.190 Million cell updates/sec

Title: US-09-331-631a-39

Perfect score: 54
Sequence: 1 CXXCXXXXXXXXXXXXXXX 22

Scoring table:
BL0SUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt; 39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#

Result No.	Score	Query Match Length	DB ID	Description
1	54	100.0	40	MTL_DROME
2	54	100.0	40	MTL_DROSI
3	54	100.0	43	MT2_DROME
4	54	100.0	47	AGRP_LURCY
5	54	100.0	55	M84C_DROME
6	54	100.0	57	MT2_SCYSE
7	54	100.0	58	MTL_HOMAM
8	54	100.0	58	MTL_SCYSE
9	54	100.0	58	MT2_CALSI
10	54	100.0	58	MTL_ASTEL
11	54	100.0	58	MTL_CARMA
12	54	100.0	58	MTL_POTPO
13	54	100.0	59	MTL_CALSI
14	54	100.0	61	MTB_HUMAN
15	54	100.0	63	M84A_DROME
16	54	100.0	64	MTL_STRPO
17	54	100.0	64	MTL_HELPD
18	54	100.0	64	MT_STENE
19	54	100.0	65	MT_PARLI
20	54	100.0	66	MTCD_HELPD
21	54	100.0	66	MT_ARIA
22	54	100.0	67	MTA_SPHGR
23	54	100.0	67	MTB_SPHGR
24	54	100.0	68	M84D_DROME
25	54	100.0	71	MT21_MYTED
26	54	100.0	71	MT22_MYTED
27	54	100.0	71	MT23_MYTED
28	54	100.0	74	M84B_DROME
29	54	100.0	74	MT_CRAVI
30	54	100.0	74	WDNM_MOUSE
31	54	100.0	74	WDMN_RAT
32	54	100.0	95	EP4_RABIT
33	54	100.0	95	YWS5_CAEEL

RESULT	1	MT1_DROME	ID	MT1_DROME STANDARD;	PRT:	40 AA.
RP	RX	RX	AC	P04357; Q9VH67;		
DT	DT	DT	DT	20-MAR-1987 (Rel. 04, created)		
DT	DT	DT	DT	20-MAR-1987 (Rel. 04, last sequence update)		
DT	DT	DT	DT	01-OCT-2000 (Rel. 04, last annotation update)		
DE	GN	GN		METALLOTHIONEIN 1 (MT-1).		
MINA	OS	OS		Drosophila melanogaster (fruit fly).		
OC	OC	OC		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.		
OC	OC	OC		[1]		
RN	RN	RN		SEQUENCE FROM N.A.		
RX	RX	RX		MEDLINE:86165787; PubMed=3007277;		
RA	RA	RA		Maroni G., Otto E., Lastowski-Perry D.;		
RT	RT	RT		"Molecular and cytogenetic characterization of a metallothionein gene of Drosophila.";		
RT	RT	RT		Genetics 112:493-504(1986).		
RL	RL	RL		[2]		
RP	RP	RP		SEQUENCE FROM N.A.		
RX	RX	RX		MEDLINE:85105016; PubMed=2578462;		
RA	RA	RA		Lastowski-Perry D., Otto E., Maroni G.;		
RT	RT	RT		"Metallothioneine sequence and expression of a Drosophila metallothionein.";		
RL	RL	RL		J. Biol. Chem. 260:1527-1530(1985).		
[3]	[3]	[3]				
SEQUENCE FROM N.A.						
RX	RX	RX		SEQUENCE FROM N.A.		
RX	RX	RX		MEDLINE:86219988; PubMed=3086075;		
RA	RA	RA		Maroni G., Lastowski-Perry D., Otto E., Watson D.;		
RT	RT	RT		"Effects of heavy metals on Drosophila larvae and a metallothionein gene.";		
RT	RT	RT		Envirion. Health Perspect. 65:107-116(1986).		
RL	RL	RL		[4]		
RN	RN	RN		SEQUENCE FROM N.A.		
RX	RX	RX		MEDLINE:88029987; PubMed=2822463;		
RA	RA	RA		Maroni G., Otto E., Lastowski-Perry D., Price D.H.;		
RT	RT	RT		"The metallothionein gene of Drosophila.";		
RL	RL	RL		Experientia Suppl. 52:385-392(1987).		
RN	RN	RN		[5]		
RP	RP	RP		SEQUENCE FROM N.A.		
RX	RX	RX		MEDLINE:92201681; PubMed=1802803;		
RA	RA	RA		Theodore L., Ho A.-S., Maroni G.;		
RT	RT	RT		"Recent evolutionary history of the metallothionein gene Mtn in Drosophila.";		
RL	RL	RL		Genet. Res. 58:203-210(1991).		
RN	RN	RN		[6]		
SEQUENCE FROM N.A.						
RC	RC	RC		SEQUENCE FROM BERKELEY;		
RX	RX	RX		MEDLINE:20196006; PubMed=10731132;		
RA	RA	RA		Adams M.D., Celinkiner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	RA	RA		Amatidiades P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	RA	RA		George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Lewellen J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champé M., Preffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,		

ALIGNMENTS

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bermudez B.P., Biandari P.D., Bolishakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burton K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew T., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.N., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Moharry C., Morris J., Moshefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nixon K.A., Nixon K., Nuskeen D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svartas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Wooley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287: 2185-2195(2000).
 RN [7]

REGULATION AND EXPRESSION.

RP MEDLINE=91012582; PubMed=1976815;

RP Silar P., Theodore L., Mokdad R., Erraiss N.-E., Cadic A., Wegnez M.;
 RT "Metallothionein Mto gene of *Drosophila melanogaster*: structure and
 regulation";
 RL J. Mol. Biol. 215:217-224(1990).

CC -!- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION ELEMENTS. IT IS THOUGHT TO BE INVOLVED IN DETOXIFICATION PROCESSES.

CC -!- INDUCTION: LATE EMBRYOGENESIS, LARVA AND ADULT.

CC -!- MISCELLANEOUS: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS.

THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER METALLOTHIONEINS.

CC -!- SIMILARITY: THE TWO DROSOPHILA METALLOTHIONEINS (MTO AND MTN) ARE ONLY 26% SIMILAR.

CC -!- SIMILARITY: BELONGS TO FAMILY 5 IN METALLOTHIONEIN SUPERFAMILY.

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CC EMBL: X03758; CAA2791.1; -

EMBL: K02114; AAA2881.1; -

EMBL: M27708; AAA2884.1; -

EMBL: M69015; AAB4134.1; -

EMBL: A003684; AAF54452.1; -

PIR: A03285; SMEF.

PIR: A25294; A25294.

HSSP: P04155; AMT2.

FLYBASE; FBgn0002868; MtNa.

INTERPRO: IPR000966; -

PRAM; PF0067; Metallothio_5; 1.

PRINTS; PR00872; MDPPTERA.

KW Metal-binding; Chelation; Copper; Cadmium; Zinc; Mercury; Polymorphism.

FT VARIANT 40 40 E -> K (IN M1NA-3);
 SQ SEQUENCE 40 AA; 3853 MN; 99A2A53CCAE634A CRC64;

Query Match 100.0%; Score 54; DB 1; Length 40;
 Best Local Similarity 18.2%; Conservative 18; Misnatches 0; Indels 0; Gaps 0;

Matches 4; PRT; 40 AA.

QY 1 CXXXCXXXXXXXCCCCXXC 22

Db 5 CGSGCKCASQATKGSCNCGSDC 26

RESULT 2

MIL_DROSI ID MTL_DROSI STANDARD; PRT; 40 AA.

AC P2254; DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-OCT-2000 (Rel. 40, Last annotation update).

DE METALLOTHIONEIN 1 (MT-1).

GN MTNA.

OS Drosophila simulans (Fruit fly), and *Drosophila ananassae* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Hydrodiidae; Drosophilidae; Drosophila.
 RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=D. SIMULANS; RX MEDLINE=91169270; PubMed=1981765;

RN Lange B.W., Langley C.H., Stephan W.H.;
 RL "Molecular evolution of *Drosophila metallothionein genes*.";
 RL Genetics 126: 921-932(1990).
 RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=D. SIMULANS; RX MEDLINE=92201681; PubMed=802803;

RC MEDLINE=95095041; PubMed=8001781;

RA Theodore L., Ho A.-S., Marion G.;
 RA Stephen W., Rodriguez V.S., Zhou B., Parsch J.;
 RA "Recent evolutionary history of the metallothionein gene Mtn in the *Drosophila*";
 RL Genet. Res. 58:203-210(1991).
 RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=D. ANANASAE; RX MEDLINE=95095041; PubMed=8001781;

CC ELEMENTS. IT IS THOUGHT TO BE INVOLVED IN DETOXIFICATION PROCESSES.

CC -!- INDUCTION: LATE EMBRYOGENESIS, LARVA AND ADULT.

CC -!- MISCELLANEOUS: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS.

THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER METALLOTHIONEINS.

CC -!- SIMILARITY: THE TWO DROSOPHILA METALLOTHIONEINS (MTO AND MTN) ARE ONLY 26% SIMILAR.

CC -!- SIMILARITY: BELONGS TO FAMILY 5 IN METALLOTHIONEIN SUPERFAMILY.

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CC EMBL: M55407; AAA03347.1; -

DR EMBL: M69016; AAA19877.1; -

DR EMBL: S75922; AAB32801.1; -

PIR; A45892; A45892.

DR	HSSP; P04355; 4M12.
DR	FLYBASE; FBgn0012845; Dsim\MtlnA.
DR	Merkulov G., Milchina N.V., Mobarrey C., Morris J., Moskaleff A., Mount S.M., Moy M., Murphy B., Murphy L., Muzay D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacleb J.M., Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos T., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Wente B., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., zhan M., Zhang G., Zhao Q., zheng L., Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "the genome sequence of <i>Drosophila melanogaster</i> "; Science 287:218-2195 (2000).
SQ	SEQUENCE 40 AA; 3852 MW; 9182A55CCAE634A CRC64;
Db	5 CGSGCKCASQATKGSCNCGSDC 26
RESULT 3	
MT2-DROME	STANDARD; PRT; 43 AA.
ID	P11956; Q9VDM2;
AC	01-OCT-1989 (Rel. 12, Created)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	METALLOTHIONEIN 2 (MT-2).
GN	MTNB OR MTO.
OS	<i>Drosophila melanogaster</i> (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hydroidea; Drosophilidae; Drosophila.
OC	[1]
RN	1
RR	SEQUENCE FROM N.A., AND SEQUENCE OF 3-27.
RC	STRAIN-OREGON-R;
RX	Medline=87204190; PubMed=3106973;
RA	Mokdad R., Debec A., Wegnez M.;
RT	"Metallothionein genes in <i>Drosophila melanogaster</i> constitute a dual system";
RL	Proc. Natl. Acad. Sci. U.S.A. 84:2658-2662(1987).
RP	[2]
RC	SEQUENCE FROM N.A., AND SEQUENCE OF 3-27.
RX	Medline=91012582; PubMed=1976815;
RA	Silar P., Theodore L., Mokdad R., Erraiss N.-E., Cadic A., Wegnez M.;
RT	"Metallothionein Mto gene of <i>Drosophila melanogaster</i> : structure and regulation";
RL	J. Mol. Biol. 215:217-224(1990).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BERKELEY;
RX	Medline=20196006; PubMed=10731132;
RA	Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gille R.F., George R.A., Lewis S.B., Richardson S., Asburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Birdwell D., Boisjoly S., Borikova D., Botchan M.R., Bouck J., Brostoller P., Brottier P., Burts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Danilevsky M., Davenport L.B., Davies P., De Pablo B., Delcher A., Deng Z., Dews I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Fosler L., Gabrielista A.C., Ferraz C., Ferreira S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Gu Z., Gund P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milchnina N.V., Mobarrey C., Morris J., Moskaleff A., Mount S.M., Moy M., Murphy B., Murphy L., Muzay D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacleb J.M., RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos T., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., SVirkas R., Tector C., Turner R., Wente B., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., zhan M., Zhang G., Zhao Q., zheng L., Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT "the genome sequence of <i>Drosophila melanogaster</i> "; Science 287:218-2195 (2000).
CC	-I- FUNCTION: THIS PROTEIN BINDS CATIONS OF SEVERAL TRANSITION ELEMENTS, THOUGHT TO BE INVOLVED IN METAL ION HOMEOSTASIS.
CC	-I- DEVELOPMENTAL STAGE: EXPRESSED PREDOMINANTLY IN EMBRYONIC AND LARVAL STAGES.
CC	-I- INDUCTION: STRONGLY INDUCED BY CADMIUM, COPPER AND MERCURY.
CC	-I- MISCELLANEOUS: ALL CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS.
CC	THESE ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER METALLOTHIONEINS.
CC	-I- SIMILARITY: THE TWO DROSOPHILA METALLOTHIONEINS (MTO AND MTN) ARE ONLY 26% SIMILAR.
CC	-I- SIMILARITY: BELONGS TO FAMILY 5 IN METALLOTHIONEIN SUPERFAMILY.
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CC	-----
DR	EMBL; M16250; AAA28683.1; -.
DR	EMBL; X52098; CAI36318.1; -.
DR	EMBL; AE003730; AAF55768.1; -.
DR	PIR; 51476; SMRF2.
DR	FLYBASE; FBgn002869; MtlnB.
DR	INTERPRO: IPR000966; -.
DR	PFAM; PF02067; Metallothio_5; 1.
DR	PRINTS; PR00872; MTDPtERA.
KW	Metal-binding; Chelation; Copper; Cadmium; Zinc.
SQ	SEQUENCE 43 AA; 4525 MW; 5EE0CF171BD9A97 CRC64;
RESULT 4	
AGRP_LUFCY	STANDARD; PRT; 47 AA.
ID	AGRP_LUFCY
AC	P56568;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	6.5 kDa ARGinine/Glutamate-rich polypeptide (6.5K-AGRP).
OS	Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
RC	[1]
RP	SEQUENCE.
RC	TISSUE=SEED;

RA	Merkulov G., Mil'shina N.V., Moarri C., Morris J., Moskrefi A.,
RA	"Primary structure of 6,5 <i>l</i> -arginine-glutamate-rich polypeptide from the seeds of sponge gourd (<i>Luffa cylindrica</i>)";
RA	Biosci. Biotechnol. Biochem. 61:984-988(1997).
RA	-!- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON RESERVES DURING GERMINATION AND SEEDLING GROWTH.
CC	-!- MASS SPECTROMETRY: MM4=569.39; METHOD=MADI.
CC	-!- SIMILARITY: SOME, TO 75 SEED STORAGE PROTEINS.
KW	seed storage protein.
FT	disulfid 12 33
FT	disulfid 16 29
SO	SEQUENCE 47 AA: 5698 MW: 588B0FCB2273AC05 CRC64;
Query Match	100.0%; Score 54; DB 1; Length 47;
Best Local Similarity	18.2%; Pred. No. 43;
Matches	4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
OY	1 CXXCXXXXXXXCXXXC 22
Db	12 CRVRCVAEHGVERORRCQVC 33
RESULT	5
ID	M84C_DROME STANDARD; PRT: 55 AA.
AC	00164; Q9VIA0; Created)
DT	01-JUL-1993 (Rel. 26, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	MALE SPECIFIC SPERM PROTEIN Mcp84DC.
GN	MST84DC.
OS	Drosophila melanogaster (Fruit fly);
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydrioidea; Drosophilidae; Drosophila.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=OREGON-R;
RX	MEDLINE=92102953; PubMed=1684716;
RX	Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,
RA	Schaefer M.;
RA	"A cluster of four genes selectively expressed in the male germ line of <i>Drosophila melanogaster</i> ";
RT	Mech. Dev. 35:143-151(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Heglins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.R., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blaszcj R.G., Champe M., Pfleiffer B.D.,
RA	Wan K.H., Doyce C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA	Abrial J.-F., Agbayani A., An H.-J., Andrews P., Pankhoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
RA	Borková D., Botchan M.R., Bouck J., Brokstein P., Brotoček P.,
RA	Burts K.C., Busam D.A., Butler H., Cadieu F., Center A., Chandra I.,
RA	Cheery J.M., Cowley S., Dahike C., Davenport L.B., Davies P.,
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraria S., Fleischmann W.,
RA	Foster C., Gabril A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernández J.R., Houck J.,
RA	Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Tai Z.,
RA	Lasko P., Lei Y., Levittky A.C., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Miller M., Park S.S., Sakai R., Yamasaki N., Funatsu G., Kimura M., Pak S.S., Saito R., Yamada T.,
RA	Mount S.M., Moy M., Murphy J., Murphy L., Muzey D.M., Nelson D.L.,
RA	Nelson D.R., Nelson J.A., Nixon K., Nusskern D.R., Pacie J.M.,
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Purji V., Reese M.G.,
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Sirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA	Williams S.M., Woodside T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT	"The genome sequence of <i>Drosophila melanogaster</i> ";
RL	Science 287:2185-2195(2000).
CC	-!- TISSUE SPECIFICITY: TESTIS
CC	-!- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES
CC	-!- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P MOTIFS
CC	-!- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/)
CC	or send an email to license@isp-sib.ch)
CC	DR EMBL: X67703; CAA47939.1; -.
DR EMBL: AE003672; AAF5205.1; -.	
DR HSP; P01880; INFO;	
DR PIYBASE; R8gn000417; Mst84DC.	
KW	Spermatogenesis; Repeat; Multigene family.
SQ	SEQUENCE 55 AA: 5225 MW: 95A12F3REC88BD6C CRC64;
Query Match	100.0%; Score 54; DB 1; Length 55;
Best Local Similarity	18.2%; Pred. No. 47;
Matches	4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
OY	1 CXXCXXXXXXXCXXXC 22
Db	15 CGCCCCGGCGCGCGCGC 36
RESULT	6
ID	MT2_SCYSE STANDARD; PRT: 57 AA.
AC	P02806; Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	METALLOTHIONEIN-1T (MM-II).
OS	Scytilia serrata (Mud crab).
OC	Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC	Eucrustacea; Decapoda; Pleocyemata; Brachyura;
OC	Brachyura; Portunoidea; Portunidae; Scyllida.
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=81412340; PubMed=7061431;
RA	Larch K., Ammer D., Olarson R.W.;
RT	"Crab metallothionein. Primary structures of metallothioneins 1 and
RT	2.;"
RL	J. Biol. Chem. 257:2420-2426(1982).
CC	-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTs IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF Elevated LEVELS OF HEAVY METAL IONS.
CC	-!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
DR	PIR: A03284; SNRDS.
DR	HSSP; P5549; IDME
DR	INTERPRO: IPR002045; -.

DR	INTERPRO; IPR003019; -.	DR	INTERPRO; IPR003019; -.
DR	PF00131; metalthio; 1.	DR	PF00131; metalthio; 1.
KW	PRINTS; PRO00858; MTICRUSTACEAN.	KW	PRINTS; PRO00858; MTICRUSTACEAN.
metal-binding; Metal-thiolate cluster; Chelation.	Metal-binding; Metal-thiolate cluster; Chelation; copper; Cadmium.	metal-binding; Metal-thiolate cluster; Chelation; copper; Cadmium.	metal-binding; Metal-thiolate cluster; Chelation; copper; Cadmium.
FT	DOMAIN 1 28	FT	DOMAIN 1 28
DOMAIN	29 57	DOMAIN	29 58
FT	METAL 4 4	FT	METAL 4 4
METAL	5 5	METAL	5 5
FT	METAL 9 9	FT	METAL 9 9
METAL	11 11	METAL	11 11
FT	METAL 16 16	FT	METAL 16 16
METAL	20 20	METAL	20 20
FT	METAL 22 22	FT	METAL 22 22
METAL	25 25	METAL	25 25
FT	METAL 27 27	FT	METAL 27 27
METAL	30 30	METAL	30 30
FT	METAL 33 33	FT	METAL 33 33
METAL	37 37	METAL	37 37
FT	METAL 39 39	FT	METAL 39 39
METAL	45 45	METAL	45 45
FT	METAL 49 49	FT	METAL 49 49
METAL	53 53	METAL	53 53
FT	METAL 55 55	FT	METAL 55 55
METAL	56 56	METAL	56 56
SQ	SEQUENCE 57 AA; 6109 MW; 8C2B3F6A6BA3611 CRC64;	SQ	SEQUENCE 58 AA; 5975 MW; 176ABA60A32F96 CRC64;
RESULT	7	RESULT	8
MTL_HOMAM	STANDARD;	MTL_SCYSE	STANDARD;
ID	PF02499;	ID	PF02805;
AC	P29499;	AC	P02805;
DT	01-APR-1993 (Rel. 25, Created)	DT	21-JUL-1986 (Rel. 01, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)	DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	METALLOTHIONEIN-1 (CMT-1).	DE	01-NOV-1997 (Rel. 35, Last annotation update)
OS	Homarus americanus (American lobster).	OS	METALLOTHIONEIN-I (Mr-I).
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropidae; Homarus.	OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura; Rubrachyura; Portunoidea; Portunidae; Scylla.
RN	[1]	RN	[1]
RP	SEQUENCE.	RP	SEQUENCE.
RC	TISSUE:HEPATOPANCREAS;	RX	MEDLINE=8215793; PubMed=2709004;
RX	MEDLINE=8215793; PubMed=2709004;	RA	Brouwer M., Winge D.R., Gray W.R.;
RA	"Structural and functional diversity of copper-metallothioneins from	RT	"Crab metallothionein. Primary structures of metallothioneins 1 and
RT	the American lobster Homarus americanus.",	RT	2";
RL	[2]	J. Inorg. Biochem. 35:289-303(1989).	J. Biol. Chem. 257:2420-2426(1982).
RP	STRUCTURE BY NMR.	CC	-I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-METAL IONS.
RX	MEDLINE=94318629; PubMed=8043573;	CC	-I- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
RA	Zhu Z., Derose E.F., Mullen G.P., Petering D.H., Shaw C.F. 111;	CC	PIR; P03283; SM0015.
RT	"Sequential proton resonance assignments and metal cluster topology of lobster metallothionein-1."	DR	DR, HSSP; P55949; 1DMF.
RT	Biochemistry 33:8858-8865(1994).	DR	INTERPRO; IPR003019; -.
CC	-I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT FORMS OF LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.	DR	INTERPRO; IPR002045; -.
CC	CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN TO BIND CADMUM.	DR	PFAM; PF00131; metalthio; 1.
CC	-I- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.	DR	PRINTS; PRO00858; MTICRUSTACEAN.
CC	CLASS I MTS IN MARINE CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-METAL IONS. BINDS 6 METAL IONS. KNOWN TO BIND CADMUM.	DR	metal-binding; metal-thiolate cluster; Chelation.
CC	-I- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.	FT	KW DOMAIN 1 28
CC	PIR; A37039; A37039.	FT	DOMAIN 29 58
CC	HSSP; P55949; 1DMF.	FT	ALPHA.
DR	INTERPRO; IPR002045; -.	FT	CLUSTER B.
DR	INTERPRO; IPR002045; -.	FT	CLUSTER B.
DR	INTERPRO; IPR002045; -.	FT	CLUSTER B.
DR	INTERPRO; IPR002045; -.	FT	CLUSTER B.

FT	METAL	16	16	CLUSTER B.
FT	METAL	20	20	CLUSTER B.
FT	METAL	22	22	CLUSTER B.
FT	METAL	25	25	CLUSTER B.
FT	METAL	27	27	CLUSTER B.
FT	METAL	30	30	CLUSTER A.
FT	METAL	33	33	CLUSTER A.
FT	METAL	37	37	CLUSTER A.
FT	METAL	39	39	CLUSTER A.
FT	METAL	45	45	CLUSTER A.
FT	METAL	49	49	CLUSTER A.
FT	METAL	53	53	CLUSTER A.
FT	METAL	55	55	CLUSTER A.
FT	METAL	56	56	CLUSTER A.
FT	SEQUENCE	58 AA;	6001 MW;	CE8A24C590B027B8 CRC64;
RESULT	9	100.0%	Score 54; DB 1; Length 58;	
Query Match		Best Local Similarity	18.2%; Pred. No. 49;	
		Matches	4; Conservative	
			18; Mismatches	
Qy	1 CXXCXXXXXXXXXXXXXXCXXC	22		
Db	16 CKEGCOCTS CRCS P EKCSSGC	37		
RESULT	10	100.0%	Score 54; DB 1; Length 58;	
MT-CALSI	STANDARD;	PRT;	58 AA.	
ID	MT2-CALSI			
AC	P55950;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA).			
OS	Callinectes sapidus (Blue crab)			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Bivalvia; Eucardida; Decapoda; Pleocyemata; Malacostrace;			
OC	Brachyura; Portunoidea; Portunidae; Callinectes.			
RN	[1]			
RP	SEQUENCE.			
RX	TISSUE=MIDGUT;			
RA	MEDLINE=907921011; PubMed=8921011;			
RA	Pedersen S.N., Pedersen K.L., Hoejrup P., Depledge M.H., Knudsen J.;			
RT	"primary structures of decapod crustacean metallothioneins with special emphasis on freshwater and semi-terrestrial species.";			
RL	Biochem. J. 319:99-1003 (1996).			
CC	-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTs IN CRUSTACEA ARE INVOLVED IN THE SEQUESTRATION OF ELEVATED LEVELS OF HEAVY-METAL IONS.			
CC	-!- INDUCTION: BY CADMIUM.			
CC	-!- MASS SPECTROMETRY: MN=5910.8; METHOD=MALDI.			
DR	HSSP: P55949, IDMD:INTERPRO; IPR002045; -.			
DR	INTERPRO; IPR002045; -.			
DR	PFAM: PF00131; metalthio: 1.			
DR	PRINTS: PRO0858; MCRUSTACEAN.			
DR	PRINTS; PRO0858; MCRUSTACEAN.			
DR	-!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.			
DR	HSSP: P55949, IDMD:INTERPRO; IPR003019; -.			
DR	INTERPRO; IPR003019; -.			
DR	PFAM: PF00131; metalthio: 1.			
DR	PRINTS: PRO0858; MCRUSTACEAN.			
DR	-!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.			
KW	Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium.			
FT	METAL-BINDING; Metal-thiolate cluster; Chelation; Cadmium.			
FT	DOMAIN 1 29 BETA.			
FT	DOMAIN 1 29 BETA.			
FT	DOMA IN 30 58 ALPHA.			
FT	DOMA IN 5 5 CLUSTER B.			
FT	DOMA IN 6 6 CLUSTER B.			
FT	DOMA IN 10 10 CLUSTER B.			
FT	DOMA IN 12 12 CLUSTER B.			
FT	DOMA IN 17 17 CLUSTER B.			
FT	DOMA IN 30 58 ALPHA.			
FT	METAL 23 23 CLUSTER B.			
FT	METAL 6 6 CLUSTER B.			
FT	METAL 10 10 CLUSTER B.			
FT	METAL 12 12 CLUSTER B.			
FT	METAL 17 17 CLUSTER B.			
FT	METAL 21 21 CLUSTER B.			
FT	METAL 23 23 CLUSTER B.			
FT	METAL 26 26 CLUSTER B.			
FT	METAL 28 28 CLUSTER B.			
FT	METAL 28 28 CLUSTER B.			
FT	METAL 31 31 CLUSTER B.			
FT	METAL 34 34 CLUSTER B.			
FT	METAL 34 34 CLUSTER B.			
FT	METAL 38 38 CLUSTER A.			
FT	METAL 21 21 CLUSTER A.			
FT	METAL 23 23 CLUSTER A.			
FT	METAL 26 26 CLUSTER A.			
FT	METAL 28 28 CLUSTER A.			
FT	METAL 31 31 CLUSTER A.			
FT	METAL 34 34 CLUSTER A.			
FT	METAL 38 38 CLUSTER A.			
FT	METAL 40 40 CLUSTER A.			
FT	METAL 46 46 CLUSTER A.			
FT	METAL 50 50 CLUSTER A.			
FT	METAL 54 54 CLUSTER A.			
FT	METAL 56 56 CLUSTER A.			
FT	SEQUENCE 58 AA;	5911 MW;	CRC64;	
FT	VARIANT 1	1	MISSING (IN VARIANT ISOLATED IN LOW CONCENTRATION);	
FT	SEQUENCE 58 AA;	5911 MW;	57635B3EE5C7122 CRC64;	
Query Match	100.0%	Score 54; DB 1; Length 58;		

DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE METALLOTHIONEIN-1 (MT-1) (MT-1B/MT-1A).
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacosirraca; Eucaridea; Decapoda; Pterygostomata; Brachyura;
OC Brachyura; Portunoidea; Portunidae; Callinectes.
RN [1]
RP
RX MEDLINE=90033052; PubMed=7487904;
RA Brouwer M., Englund J., Hoekum-Brouwer T., Thøgersen I., Truncali A.;
RT "Primary structure and tissue-specific expression of blue crab
RT (Callinectes sapidus) metallothionein isoforms.";
RL Biochem. J. 311:617-622(1995).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=931119049; PubMed=7819257;
RA Narula S., Brouwer M., Hua Y., Armitage I.M.;
RT "Three-dimensional solution structure of Callinectes sapidus
RT metallothionein-1 determined by homonuclear and heteronuclear
RT magnetic resonance spectroscopy.";
RL Biochemistry 34:620-631(1995).
CC -I- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
CC CADMIUM.
CC !- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
PDB: 1DMC; 07-FEB-95.
DR PDB: 1DMD; 07-FEB-95.
DR PDB: 1DME; 07-FEB-95.
DR PDB: 1DMF; 07-FEB-95.
INTERPRO: IPR002045; -.
DR PFAM: PF00131; metathio; 1.
DR PRINTS; PRO0858; MTRUSTACLEAN.
KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium;
KW 3D-structure.
FT DOMAIN 1 29 BETA.
FT PT METAL 5 59 ALPHA.
FT PT METAL 5 5 CLUSTER B.
FT PT METAL 6 6 CLUSTER B.
FT PT METAL 10 10 CLUSTER B.
FT PT METAL 12 12 CLUSTER B.
FT PT METAL 17 17 CLUSTER B.
FT PT METAL 21 21 CLUSTER B.
FT PT METAL 23 23 CLUSTER B.
FT PT METAL 26 26 CLUSTER B.
FT PT METAL 28 28 CLUSTER B.
FT PT METAL 31 31 CLUSTER A.
FT PT METAL 34 34 CLUSTER A.
FT PT METAL 38 38 CLUSTER A.
FT PT METAL 40 40 CLUSTER A.
FT PT METAL 46 46 CLUSTER A.
FT PT METAL 50 50 CLUSTER A.
FT PT METAL 54 54 CLUSTER A.
FT PT METAL 56 56 CLUSTER A.
FT PT METAL 57 57 CLUSTER A.
FT PT VARIANT 1 1 MISSING (IN MT-1A).
SQ SEQUENCE 59 AA; 6141 MW; 4398B0A9D1A96D34 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 59;
Best Local Similarity 18.2%; Pred. No. 49; Length 59;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXX 22
ID |::|::|::|::|::|::|::|:
Db 17 CKAGGQCTSCRCSPQKCISGC 38

RESULT 14
ID MT1B_HUMAN STANDARD PRT 61 AA.
AC P07438;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE METALLOTHIONEIN-1B (MT-1B).
GN MT1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoide; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=87064506; PubMed=3785191;
RA Heguy A., West A., Richards R.I., Karin M.;
RT "Structure and tissue-specific expression of the human
RT metallothionein 1B gene.";
RL Mol. Cell. Biol. 6:2149-2157(1986).
CC -I- FUNCTION: METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS.
CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
CC GLUCOCORTICOIDS.
CC -I- SUBUNIT: MONOMER.
CC FOUR DIVALENT METAL IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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CC -----
DR EMBL; MI3485; AAA36331.1; -.
DR EMBL; MI3484; AAA36331.1; JOINED.
DR PIR; A25244; A25244.
DR HSSP; P04355; 2NRT.
DR MIM; 156349; -.
DR INTERPRO; IPR000006; -.
DR INTERPRO; IPR003019; -.
DR PFAM; PF00131; metathio; 1.
DR PRINTS; PRO0860; MTRVERTERB.
KW PROSITE; PS00203; METALLOTHIONEIN_VTR; 1.
KW Metal-binding; Metal-thiolate cluster; Chelation; Zinc; Copper;
KW Cadmium; Acetylation.
FT MOD-RES 1 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 1 29 ALPHA.
FT PT METAL 30 61 CLUSTER B.
FT PT METAL 5 5 CLUSTER B.
FT PT METAL 7 7 CLUSTER B.
FT PT METAL 13 13 CLUSTER B.
FT PT METAL 15 15 CLUSTER B.
FT PT METAL 19 19 CLUSTER B.
FT PT METAL 21 21 CLUSTER B.
FT PT METAL 24 24 CLUSTER B.
FT PT METAL 26 26 CLUSTER B.
FT PT METAL 29 29 CLUSTER B.
FT PT METAL 33 33 CLUSTER A.
FT PT METAL 34 34 CLUSTER A.
FT PT METAL 36 36 CLUSTER A.
FT PT METAL 37 37 CLUSTER A.
FT PT METAL 41 41 CLUSTER A.
FT PT METAL 44 44 CLUSTER A.
FT PT METAL 48 48 CLUSTER A.
FT PT METAL 50 50 CLUSTER A.
FT PT METAL 57 57 CLUSTER A.
FT PT METAL 59 59 CLUSTER A.
FT PT METAL 60 60 CLUSTER A.
SQ SEQUENCE 61 AA; 6115 MW; 8DC566E5462810D3 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 61;
Best Local Similarity 18.2%; Pred. No. 51; Length 61;

<p>Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;</p> <p>Qy 1 CXXXCXXXXXXXXXXXX 22 ::: ::: ::: ::: ::: : Db 15 CAGSCKCKECKCTSKKCCSC 36</p> <p>RESULT 15</p> <p>M84A_DROME M84A_DROME STANDARD; PRT; 63 AA.</p> <p>ID M84A_DROME STANDARD; PRT; 63 AA.</p> <p>AC 001642; O9VIA3; DT 01-JUL-1993 (Rel. 26, Created) DT 01-JUL-1993 (Rel. 26, Last sequence update) DE MALE SPECIFIC SPERM PROTEIN MST84DA.</p> <p>GN MST84DA.</p> <p>OS Drosophila melanogaster (Fruit fly).</p> <p>OC Eukaryota; Metacoa; Arthropoda; Diptera; Brachycera; Insecta; Pterygota; Neoptera; Endopterygota; Drosophilidae; Drosophila.</p> <p>OC Ephdroidea; Drosophilidae; Drosophila.</p> <p>RN [1]</p> <p>RP SEQUENCE FROM N.A.</p> <p>RC STRAIN=ORECON-R;</p> <p>RX MEDLINE=92102953; PubMed=1684716;</p> <p>RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaeffer U., Schaefer M.; " A cluster of four genes selectively expressed in the male germ line of Drosophila melanogaster. "; Mech. Dev. 35:143-151(1991). [2]</p> <p>RN RP SEQUENCE FROM N.A.</p> <p>RC STRAIN=BERKELEY;</p> <p>RX MEDLINE=20196006; PubMed=10731132;</p> <p>RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amannidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champs M., Pfeiffer B.D., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., Abriel J.F., Agayamani A., An H.-J., Andrews-Pflanck C., Baldwin D., Raabe A., Basu A., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.J., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brodstein P., Brodtier P., Brotzler P., Burtis K.C., Busam D.A., Butler H., Cadile E., Centor A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.M., Ebrango-ista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeewam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moslurefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.R., Nelson K.A., Nixon D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinhart K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamo T., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Yaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L., Zheng X.H., Zhong P., Zhou W., Zhou X., Zhu S., Zhu X., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., RT RT The genome sequence of Drosophila melanogaster.";</p> <p>CC CC -!- TISSUE SPECIFICITY: TESTIS. CC CC -!- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.</p>	<p>CC !- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P MOTIFS.</p> <p>CC !- SIMILARITY: BELONGS TO THE MST (3)CGP FAMILY.</p> <p>CC -----</p> <p>CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).</p> <p>CC -----</p> <p>CC DR EMBL; X67703; CAA47937; 1; -</p> <p>CC DR EMBL; AE003672; AAF54022; 1; -</p> <p>DR ISSN; P01180; INPO.</p> <p>DR FLYBASE; FBgn0004172; Ms184Da.</p> <p>KW SPERMATOGENESIS; Repeat; Multigene family.</p> <p>SO SEQUENCE 63 AA; 5806 MW; BR84C074CBEBFD3F CRC64;</p> <p>Query Match 100.0%; Score 54; DB 1; Length 63;</p> <p>Best Local Similarity 18.2%; Pred. No. 52;</p> <p>Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;</p> <p>Qy 1 CXXXCXXXXXXXXXXXX 22 ::: ::: ::: ::: ::: : Db 29 CGPCCGGCGPCGPGCGCGGCC 50</p>
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Search completed: March 1, 2001, 16:26:04
Job time: 401 sec

